

What is Life?

Daniel Sander Hoffmann im Gespräch mit Bernd-Olaf Küppers

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Episteme: Thank you very much for kindly accepting to participate in this interview, Dr. Küppers. You are member of the scientific board of the journal "Selbstorganisation". In an interview to Episteme, the philosopher of biology Michael Ruse said explicitly that the concept of self-organization in biology is "bullshit", and that this in a sense signs the return of vitalism. But in your work you do emphasize both the importance of self-organization and the error of vitalism. May you please comment on this subject? What is self-organization, after all?

Küppers: I do not understand the objections of Michael Ruse. The concept of self-organization is one of the most important concepts of modern biology. It essentially claims that - given the appropriate substances - living systems can organize themselves on the basis of the known laws of physics and chemistry. This is the basic idea underlying the physicochemical theory of the origin and evolution of life which I have outlined some years ago in my book Molecular Theory of Evolution. The concept of self-organization is part of the so-called „reductionistic research programme“ which pursues the goal to reduce all properties and phenomena of the living to physical and chemical processes. There is no mysterious element in it which could justify the suspicion of Michael Ruse that the concept of self-organization represents a return to the old fashioned idea of vitalism. Let me add another point. The quality of a scientific concept is not a question of philosophy, ideology or sympathy. It can only be judged according to its capacity to solve problems. In this respect the concept of self-organization turns out to be indispensable for an adequate explanation of the origin and early evolution of life. However in order to understand in detail what „self-organization“ means we have to consider in more detail the problem of biological organization. The most significant property of the living is its enormous degree of material organization. This exceeds all orders of complexity which are known from non-living matter. Thus in the first half of the 20th century many physicists believed that the phenomenon of biological organization can only be explained by the action of new, but unknown laws. For this reason some physicists like Max Delbrück gave up physics in favour of biology because they had the hope to find the unknown laws which were supposed to govern the living. Those physicists did

a lot of brilliant work in biology, but they never found any new physical or chemical law. This failure indicates that there must be another source for the complexity of the living. Today we know that the complete organizational structure of a living system is encoded in its „boundaries“. The boundaries can be considered as physical constraints which act on the physical and chemical laws. They have the function of selection conditions, which narrow down the range of possible physical processes to those which are actually going on in the system - in the same way as a pearl bounded to a wire can only move in one dimension. In fact the living system is determined by a complex hierarchy of boundaries. However more astonishing is the fact that all boundaries of the living organism are themselves encoded in a primary boundary, the genome. These primary boundaries are represented by macromolecular structures like the DNA or RNA molecules. Thus in order to understand the origin and evolution of life we have to understand the origin and evolution of specific, i.e. non-contingent physical boundaries starting from some unspecific, i.e. contingent physical conditions. There are convincing models that in open systems involving some kind of dynamical feed back this evolutionary process can take place spontaneously whereby the boundaries modify themselves step by step. This the deeper meaning of the concept of „self-organisation“.

Episteme: In a paper entitled "Understanding Complexity", you wrote at the introduction that "the reductionistic research programme starts from the epistemological premises that there is no principal difference between non-living and living matter, and that the transition from the non-living to the living must be considered as a quasi-continuous one, in which no other principles are involved than the general principles of physics and chemistry" (p. 241). Perhaps you may provide a technical clarification at this point.

Küppers: It is impossible to do scientific research without accepting some epistemological premisses and methodological rules. For example to the standards of the scientific method belongs the analytical procedure. According to this strategy, which actually goes back to Descartes and Newton, one has to decompose a system into fragments in order to understand the whole from the interactions of its parts. Any causal explanation in science requires such analytical steps. These are necessary in order to identify in a network of interactions „causes“ and „effects“. Another methodological criterium is that of simplicity. It claims that one should always try to minimize the number of assumptions and preconditions. Following this rule one should always strive to explain living systems within the framework of physics

and chemistry and one should avoid to introduce any new forces, principles, laws etc which are outside the realm of physics. The reductionistic research programme follows exactly these methodological rules. It starts with the premise that there is no principle difference between the non-living and the living and that all phenomena of the living could be - at least in principle - reduced analytically to the interaction of physical and chemical processes.

Episteme: In the same paper, you wrote that "one has to give up the idea that the phenomena of emergence and downward causation at once emerge when matter reaches a certain level of complexity. Instead, both phenomena must be thought of as epiphenomena of self-organizing matter that continuously emerge when matter unfolds its complexity by organizing itself." Can you explain this for the tourist?

Küppers: Let me first explain what „emergence“ and „downward causation“ means. The first term „emergence“ denotes a phenomenon which can be described by the popular phrase: „The whole is more than the sum of its parts“. The second term „downward causation“ represents in a certain sense the dynamical complement of the first phrase: „The whole determines the behaviour of the parts“. Some philosophers of biology believe that both phrases refer to some irreducible aspects of living matter and that the aspects of „wholeness“ demonstrate the limitations of the reductionistic research programme. However it can be shown that „emergence“ and „downward causation“ denote phenomena which „emerge“ at all levels of reality, from atoms to living organisms, and that both phenomena can be very well explained within the framework of physics and chemistry. In my book *Information and The Origin of Life* you will find the corresponding examples. The examples, taken from physics and chemistry, demonstrate very clearly that „emergence“ and „downward causation“ can not be considered to characterize any ontological or epistemological difference between living and non-living matter

Episteme: What is complexity? Do you consider "complexity" and "complication" synonymous?

Küppers: The question „What is complexity?“ is very difficult. This is mainly due to the fact

that there are a number of quite different meanings associated with the word „complexity“. Nevertheless there is a mathematical concept, the theory of algorithmic complexity, which gives the notion of complexity a precise meaning and which can be applied to a wide range of phenomena. This theory which has been developed independently by Solomonoff, Kolmogorov and Chaitin takes the fact into account that the „complexity“ of a structure has something to do with its incompressibility. The basic idea of this concept can be at best demonstrated with the help of a biological example. Let us consider the structure of a DNA molecule which encodes some genetic information. This DNA is build up of four classes of nucleotides (A, T, G and C) and can be represented by a complex series of binary digits. Now we can ask whether those sequences can be generated by simple algorithms, i.e. by algorithms that are less complex than the sequences itself. Obviously, we can only expect to find an algorithm if the sequence is non-random. As long as we do not find such an algorithm we consider the corresponding sequence to be incompressible. It may be the case that there is in fact no algorithm at all. But this cannot be proven because one never can prove the non-existence of something. But as soon as we find an appropriate, i.e. shorter algorithm, the sequence - generated by this algorithm - turns out to be „complicate“, but no longer as „complex“ as before. Thus the statement that a given sequence is of inherent complexity can only be formulated as a hypothetical statement. To summarize the answer to your second question: the notion of „complicate“ is an epistemological one, that of „complex“ is an ontological one.

Episteme: What is information? How do you see the relative importance of Shannon's theory of information and the algorithmic information theory? What are their differences and what do they have in common?

Küppers: The algorithmic theory of complexity can be applied to binary strings which may be potential carriers of information. Therefore this theory is also called „algorithmic information theory“. The most characteristic difference between Shannon's information theory and algorithmic information theory can be described as following: Information - according to Shannon - has to remove uncertainty. Therefore it was a consequent idea of Shannon to put the measure of information into a reciprocal relationship to its expectation probability. In other words: the lower the expectation probability for a message is the higher is its information contents if this message is received by the receiver. Thus Shannons measure of information

always refers to a source of information. It is necessarily defined on a probability distribution which describes the expectation values for all potential informations which may originate from this source. However within the frame-work of algorithmic information theory the information contents is measured by the incompressibility of the individual information carrier. This concept describes much better the complexity encoded by genetic information than the Shannon information. Some years ago I applied the concept of algorithmic information theory for the first time to the problem of the origin and evolution of life in order to clarify and dissolve a number of fundamental epistemological questions. I think that the application of algorithmic theory in biology has lead to a real breakthrough in the information theoretical foundation of biology. For a comprehensive representation of the theory I would like to refer again to my book *Information and the Origin of Life*.

Episteme: What is life?

Küppers: An answer to the question „What is life?“ depends in a crucial way from the question whether there is a sharp borderline between the living and the non-living or not. Let us first consider the case that there is a sharp border between living and non-living matter. In this case one can (in principle) give necessary and sufficient criteria for the definition of life. But in order to achieve a complete definition one has to pay a high price. For, every complete definition involves at least one criterium which describes the ontological difference between the non-living and the living and which for fundamental reasons can not be reduced to physical properties of matter. In this case life is being defined by some criterium that is specific for the living. In other words: Every „complete“ definition of life is irreducible and thereby tautological. Let us now consider the alternative case. Let us assume that there is no sharp border between living and non-living matter and that the transition from the non-living to the „living“ is a quasi-continuous one. In this case the definition can only involve necessary but no sufficient criteria. Thus, for principle reasons the definition must be incomplete and it is more or less arbitrary which objects we call alive or not. The definition depends exclusively from the scientific perspective we adopt. For example, a biochemist might call a system already alive if it can reproduce itself, if it shows some metabolism (i.e. turnover of free energy) and if it is subject of mutations. A cell biologist certainly will list further properties, especially that of compartmentation. And I suppose that a neurobiologist will call a system alive if it shows some primitive neural organization. The problem of

defining life demonstrates that we can only do science within the framework of abstractions. However in the present case this leads to a paradoxal situation. In order to give a complete physical description of the origin of life we have to assume that the transition from the non-living to the living is a quasi-continuous one. But in this case we necessarily have to work with an incomplete definition of life.

Episteme: How do you see the research in artificial life?

Küppers: This research field is an interesting application of the concept of self-organization. It has essentially two experimental branches. One is dealing with the processes of self-organization and evolution in vitro. This branch of artificial life has been initiated by Sol Spiegelman and his co-workers with their classical experiments on the evolution of the Q β -genome in the test tube. I myself have been involved in this kind of experimental studies during the early seventies. During the last twenty years these techniques have developed into a new type of biotechnology which is called „artificial evolution“. By this technology the principles of life are simulated under experimental control in order to generate and optimize biochemical substances which are not found in Nature. The other branch of artificial life studies self-organizing processes with the help of computer simulations. Those experiments have many theoretical and practical implications for the computer sciences. But they are also important in order to learn more about the general principles of self-organization and evolution of complex structures.

Episteme: Do you accept the "strong version" of Alive, that says that virtual creatures are really alive?

Küppers: Since life has been developed on earth only once we have no independent criterium for the definition of life. Thus following the reductio-nistic research programme every definition of life involves a normative aspect which denotes the demarcation line between the non-living and the living. Therefore every notion of „alive“ has to be relativized to the point where we intend to make the cut between the living and the non-living. As I have outlined before the demarcation line is more or less arbitrarily because it depends on the scientific perspective one adopts with respect to a living system. Thus it is a matter of taste which

difference between the authentic forms of life and their artificial derivatives you are willing to accept.

Episteme: And what about the meaning of computer simulations in silico, or computer experiments?

Küppers: There is no doubt that computer experiments play an outstanding role in modern sciences. They have already replaced to a considerable extent the classical physical experiment. Especially in the life sciences where we are dealing with systems of extraordinary complexity computer simulations are indispensable. Nevertheless we have to be aware of the fact that computer experiments only simulate the reality but that they never represent the reality itself. There always exists the latent danger to generate some kind of pseudoreality or virtual reality due to the misinterpretation and overinterpretation of data resulting from computer experiments. Therefore one has to be very sensitive and critical with respect to the cognitive values of computer experiments.

Episteme: Would you consider that "biomathematics" has, or will ever reach, the status of an independent discipline, as some thinkers seem to suggest?

Küppers: Biomathematics are not a mere application of mathematical techniques to biological problems. Instead biomathematics must be considered as an autonomous or better „semi-autonomous“ scientific discipline which includes very important branches of applied mathematics like cybernetics, game theory, information theory, catastrophe theory, systems theory etc. These are scientific disciplines which belong to the wide range of structural sciences. Besides traditional physics and chemistry the structural sciences build the skeleton for the theoretical foundation of biology. Moreover the growing importance of the structural sciences for the understanding of complexity indicates an interesting paradigm shift in modern science. It is the shift from the properties of matter which are the main subject of investigations in traditional physics and chemistry to the functional relationships between abstract structures.

Episteme: In your viewpoint, what specific problems are still waiting for a solution in theoretical science and in the philosophy of science?

Küppers: It is a truism that every solution of a scientific problem induces at least two new problems. This is the progressive character of scientific discovery and there seems to be no end of this process. Thus it makes no sense to pick up an individual problem which is still waiting for a solution. Instead let me try to sketch the general scenario for future research. Moreo-ver I will restrict my consideration to my own scientific domain, i.e. evolutionary biology. But let me first describe the present stage of research. There is no doubt that the Darwinian concept of evolution (including modern genetics) is the best theoretical concept we have in biology. It verifies the famous statement of Theodosius Dobzhansky that „nothing in biology makes sense except in the light of evolution“. In fact the Darwinian concept of evolution is as important for modern biology as Newtonian physics have been for the development of modern physics. But as in the case of Newtonian physics we can not expect that the Darwinian concept will be the last word. The history of science demonstrates quite clearly that all basic concepts of the natural sciences have later been improved upon. And indeed there still exist some riddles of evolutionary biology which up to now have not yet found a satisfying solution. Let me enlarge a little bit on this point: Molecular biology has shown that all life processes can be interpreted in terms of storage, transmission, processing and generation of information. Even the Darwinian concept itself can be translated into the language of information theory so that we can reformulate Dobzhansky's statement by saying that „nothing in biology makes sense except in the light of information“. But if we look carefully to the concept of information we note that information in an absolute sense does not exist. Information is always related to some other information or information-carrying context. In view of this fact we must ask whether genetic information can be generated out from nothing as the Darwinian theory seems to imply. At the moment we can only speculate about the answer. However some results from my recent research indicate that the answer will be „no“. If this turns out to be true we have to modify our common understanding of evolution. In this case the evolutionary development of genetic information can no longer be considered as a process of generation of information out from nothing. Instead the process must be considered as a process of unfolding and permanent trans-formation of information in a complex environment. However a rigorous approach to this problem requires a theoretical foundation of the semantic aspect of information. But the notion of „semantics“ exceeds the traditional framework of natural sciences and we have to look for new pathways. Again, algorithmic information theory seems to offer some promising beginnings. These are the

problems I am interested in at present.

Episteme: Who is Bernd-Olaf Küppers (Küppers as described by himself) in a few words?

Küppers: In a German newspaper a journalist once called me to be a „border crosser“. I think that this is a very good characterization of my scientific personality. In fact, if we are going to approach such a fundamental problem of science like that of the origin of life we have to cross again and again the borders between the scientific disciplines. And sometimes we have to go completely new pathways nobody has gone before. This requires not only imagination and unconventional ideas, but above all a lot of self-confidence and courage.

Episteme: Thank you very much for giving us the opportunity of knowing more about your life and work.